B. O'Laughlin.

RAW SEQUENCE LISTING   DATE: 09/27/2000
PATENT APPLICATION: US/09/492,028   TIME: 15:37:23

Input Set : A:\Uc-926-1.app
Output Set: N:\CRF3\09272000\I492028.raw

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 3  <110> APPLICANT: Zuker, Charles S.
 4         The Regents of the University of California
 6  <120> TITLE OF INVENTION: Assays for Sensory Modulators Using a Sensory Cell
 7         Specific G-Protein Alpha Subunit
 9  <130> FILE REFERENCE: 02307E-092610US
11  <140> CURRENT APPLICATION NUMBER: US 09/492,028
12  <141> CURRENT FILING DATE: 2000-01-26
14  <150> PRIOR APPLICATION NUMBER: US 60/117,367
15  <151> PRIOR FILING DATE: 1999-01-27
17  <160> NUMBER OF SEQ ID NOS: 2
19  <170> SOFTWARE: PatentIn Ver. 2.1
21  <210> SEQ ID NO: 1
22  <211> LENGTH: 1503
23  <212> TYPE: DNA
24  <213> ORGANISM: Mus sp.
26  <220> FEATURE:
27  <221> NAME/KEY: CDS
28  <222> LOCATION: (157)..(1224)
29  <223> OTHER INFORMATION: mouse taste cell specific G-protein alpha 14
30         subunit (TC-Galpha14)
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35  tcaggtggtt tcctcttcaa accttgcgtc tgcggataat ccgcgcggcc gggcgttaag  120
37  ctccaggtcc ctgtcgctcc gtcgaggtgg caagcc atg gcc ggc tgc tgc tgt   174
38                                         Met Ala Gly Cys Cys Cys
39                                          1               5
41  ttg tct gcg gag gag aaa gag tct cag cgc atc agc gcg gag atc gag   222
42  Leu Ser Ala Glu Glu Lys Glu Ser Gln Arg Ile Ser Ala Glu Ile Glu
43              10              15                  20
45  cgg cac gtt cgc cgc gac aag aag gac gcg cgc cgg gag ctc aag ctg   270
46  Arg His Val Arg Arg Asp Lys Lys Asp Ala Arg Arg Glu Leu Lys Leu
47              25              30                  35
49  ctg ttg ctg gga acc ggt gag agt ggg aaa agc acc ttt atc aag cag   318
50  Leu Leu Leu Gly Thr Gly Glu Ser Gly Lys Ser Thr Phe Ile Lys Gln
51              40              45                  50
53  atg agg ata atc cat ggg tct ggc tac agt gat gaa gat aga aag ggc   366
54  Met Arg Ile Ile His Gly Ser Gly Tyr Ser Asp Glu Asp Arg Lys Gly
55   55              60                  65                  70
57  ttc acg aag ctg gtt tac caa aac ata ttc acg gcc atg caa gcc atg   414
58  Phe Thr Lys Leu Val Tyr Gln Asn Ile Phe Thr Ala Met Gln Ala Met
59                  75                  80                  85
61  atc aga gca atg gat acc ctg agg ata caa tac atg tgt gag cag aat   462
62  Ile Arg Ala Met Asp Thr Leu Arg Ile Gln Tyr Met Cys Glu Gln Asn
63              90                  95                  100
65  aag gaa aat gcc cag atc atc agg gaa gtg gaa gta gac aag gtc act   510
66  Lys Glu Asn Ala Gln Ile Ile Arg Glu Val Glu Val Asp Lys Val Thr
67              105                 110                 115
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 69 gca ctc tct aga gac cag gtg gca gcc atc aag cag ctg tgg ctg gat   558
 70 Ala Leu Ser Arg Asp Gln Val Ala Ala Ile Lys Gln Leu Trp Leu Asp
 71     120             125             130
 73 ccc gga atc cag gag tgt tac gac agg agg agg gag tac cag ctg tca   606
 74 Pro Gly Ile Gln Glu Cys Tyr Asp Arg Arg Arg Glu Tyr Gln Leu Ser
 75 135             140             145             150
 77 gac tct gcc aaa tat tac ctg acg gac att gag cgt atc gcc atg ccc   654
 78 Asp Ser Ala Lys Tyr Tyr Leu Thr Asp Ile Glu Arg Ile Ala Met Pro
 79             155             160             165
 81 tct ttc gtg cca aca caa cag gat gtg ctt cgt gtt aga gtg ccc acc   702
 82 Ser Phe Val Pro Thr Gln Gln Asp Val Leu Arg Val Arg Val Pro Thr
 83             170             175             180
 85 act ggc atc ata gaa tat cca ttc gac ctg gaa aac atc atc ttc cga   750
 86 Thr Gly Ile Ile Glu Tyr Pro Phe Asp Leu Glu Asn Ile Ile Phe Arg
 87         185             190             195
 89 atg gtg gat gtt ggt ggc cag cga tct gaa cga cgg aaa tgg att cac   798
 90 Met Val Asp Val Gly Gly Gln Arg Ser Glu Arg Arg Lys Trp Ile His
 91     200             205             210
 93 tgc ttt gag agt gtc acc tcc atc att ttc ttg gtt gct ctg agt gaa   846
 94 Cys Phe Glu Ser Val Thr Ser Ile Ile Phe Leu Val Ala Leu Ser Glu
 95 215             220             225             230
 97 tat gac cag gtt ctg gct gag tgt gac aat gag aac cgc atg gag gag   894
 98 Tyr Asp Gln Val Leu Ala Glu Cys Asp Asn Glu Asn Arg Met Glu Glu
 99             235             240             245
101 agc aaa gcc ctg ttt aga acc atc atc acc tac ccc tgg ttt ctg aac   942
102 Ser Lys Ala Leu Phe Arg Thr Ile Ile Thr Tyr Pro Trp Phe Leu Asn
103             250             255             260
105 tcc tcc gtg att ctg ttc tta aac aag aag gat ctt cta gag gag aaa   990
106 Ser Ser Val Ile Leu Phe Leu Asn Lys Lys Asp Leu Leu Glu Glu Lys
107             265             270             275
109 atc atg tac tct cat cta att agc tac ttc cca gag tac aca gga cca  1038
110 Ile Met Tyr Ser His Leu Ile Ser Tyr Phe Pro Glu Tyr Thr Gly Pro
111     280             285             290
113 aag caa gat gtc aaa gcg gcc agg gac ttt atc ctg aag ctg tat caa  1086
114 Lys Gln Asp Val Lys Ala Ala Arg Asp Phe Ile Leu Lys Leu Tyr Gln
115 295             300             305             310
117 gac cag aat cct gac aaa gag aag gtt atc tat tct cac ttc act tgt  1134
118 Asp Gln Asn Pro Asp Lys Glu Lys Val Ile Tyr Ser His Phe Thr Cys
119             315             320             325
121 gct aca gac acc gag aat atc cgc ttt gtg ttt gct gct gtc aaa gac  1182
122 Ala Thr Asp Thr Glu Asn Ile Arg Phe Val Phe Ala Ala Val Lys Asp
123             330             335             340
125 aca atc cta cag cta aac cta cgg gag ttc aac ttg gtg taa         1224
126 Thr Ile Leu Gln Leu Asn Leu Arg Glu Phe Asn Leu Val
127         345             350             355
129 atggagggcc tactcctccg agacagaggg tgatctgagc ccttcctgcc tgatctacaa 1284
131 gtgcttctgg accaggacct aaggacatta tgtagcccac aggacagaga tgggtagtgc 1344
133 aatgtgaaaa atacttcacc aacccttta agtgtcttta attcttcact gtctaactct 1404
135 tttctcgcct tttggttgaa cgattaggta tcattttga gtggttcccc ctctcctatt 1464
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140 <210> SEQ ID NO: 2
141 <211> LENGTH: 355
142 <212> TYPE: PRT
143 <213> ORGANISM: Mus sp.
145 <400> SEQUENCE: 2
146 Met Ala Gly Cys Cys Cys Leu Ser Ala Glu Glu Lys Glu Ser Gln Arg
147  1               5                  10                  15
148 Ile Ser Ala Glu Ile Glu Arg His Val Arg Arg Asp Lys Lys Asp Ala
149             20                  25                  30
150 Arg Arg Glu Leu Lys Leu Leu Leu Leu Gly Thr Gly Glu Ser Gly Lys
151         35                  40                  45
152 Ser Thr Phe Ile Lys Gln Met Arg Ile Ile His Gly Ser Gly Tyr Ser
153         50                  55                  60
154 Asp Glu Asp Arg Lys Gly Phe Thr Lys Leu Val Tyr Gln Asn Ile Phe
155  65                  70                  75                  80
156 Thr Ala Met Gln Ala Met Ile Arg Ala Met Asp Thr Leu Arg Ile Gln
157             85                  90                  95
158 Tyr Met Cys Glu Gln Asn Lys Glu Asn Ala Gln Ile Ile Arg Glu Val
159             100                 105                 110
160 Glu Val Asp Lys Val Thr Ala Leu Ser Arg Asp Gln Val Ala Ala Ile
161         115                 120                 125
162 Lys Gln Leu Trp Leu Asp Pro Gly Ile Gln Glu Cys Tyr Asp Arg Arg
163     130                 135                 140
164 Arg Glu Tyr Gln Leu Ser Asp Ser Ala Lys Tyr Tyr Leu Thr Asp Ile
165 145                 150                 155                 160
166 Glu Arg Ile Ala Met Pro Ser Phe Val Pro Thr Gln Gln Asp Val Leu
167             165                 170                 175
168 Arg Val Arg Val Pro Thr Thr Gly Ile Ile Glu Tyr Pro Phe Asp Leu
169             180                 185                 190
170 Glu Asn Ile Ile Phe Arg Met Val Asp Val Gly Gly Gln Arg Ser Glu
171         195                 200                 205
172 Arg Arg Lys Trp Ile His Cys Phe Glu Ser Val Thr Ser Ile Ile Phe
173     210                 215                 220
174 Leu Val Ala Leu Ser Glu Tyr Asp Gln Val Leu Ala Glu Cys Asp Asn
175 225                 230                 235                 240
176 Glu Asn Arg Met Glu Glu Ser Lys Ala Leu Phe Arg Thr Ile Ile Thr
177             245                 250                 255
178 Tyr Pro Trp Phe Leu Asn Ser Ser Val Ile Leu Phe Leu Asn Lys Lys
179             260                 265                 270
180 Asp Leu Leu Glu Glu Lys Ile Met Tyr Ser His Leu Ile Ser Tyr Phe
181         275                 280                 285
182 Pro Glu Tyr Thr Gly Pro Lys Gln Asp Val Lys Ala Ala Arg Asp Phe
183     290                 295                 300
184 Ile Leu Lys Leu Tyr Gln Asp Gln Asn Pro Asp Lys Glu Lys Val Ile
185 305                 310                 315                 320
186 Tyr Ser His Phe Thr Cys Ala Thr Asp Thr Glu Asn Ile Arg Phe Val
187             325                 330                 335
188 Phe Ala Ala Val Lys Asp Thr Ile Leu Gln Leu Asn Leu Arg Glu Phe
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189            340              345              350.
190 Asn Leu Val
191            355
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VERIFICATION SUMMARY   DATE: 09/27/2000
PATENT APPLICATION: US/09/492,028 TIME: 15:37:24

Input Set : A:\Uc-926-1.app
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